

1817 (corresponding to SEQ ID NO:3); PTA-2635 (corresponding to SEQ ID NO:9); PTA-2634 (comprising SEQ ID NO:27); and PTA-2636 (comprising SEQ ID NO:28).

In The Claims:

Please amend the claims as follows:

1. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:
- (a) a nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 15, or 17;
 - (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 16, or 18;
 - (c) a nucleotide sequence characterized by at least 88% sequence identity to the nucleotide sequence set forth in (a);
 - (d) a nucleotide sequence encoding a protein comprising an amino acid sequence characterized by at least 85% sequence identity to the amino acid sequence set forth in (b);
 - (e) an antisense nucleotide sequence corresponding to a nucleotide sequence of any one of (a) to (d); and
 - (f) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of (a).

2. The polypeptide according to claim 4, wherein said polypeptide is characterized by pesticidal activity against at least one pest belonging to the order Coleoptera.

3. The method according to claim 7, wherein said insect pest is selected from the group consisting of Colorado potato beetle, western corn rootworm, southern corn rootworm, and boll weevil.

4. A transformed plant comprising in its genome at least one stably

incorporated nucleotide construct comprising a coding sequence operably linked to a promoter that drives expression of a polypeptide that is pesticidal for at least one pest belonging to the order Coleoptera, wherein said coding sequence is selected from the group consisting of:

- a3
- (a) a nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 15, or 17;
 - (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 16, or 18;
 - (c) a nucleotide sequence characterized by at least 88% sequence identity to the nucleotide sequence set forth in (a);
 - (d) a nucleotide sequence encoding a protein comprising an amino acid sequence characterized by at least 85% sequence identity to the amino acid sequence set forth in (b);
 - (e) a nucleotide sequence according to any one of (a) to (d) that comprises codons optimized for expression in a plant;
 - (f) an antisense nucleotide sequence corresponding to a nucleotide sequence of any one of (a) to (d); and
 - (g) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of (a).

13. A transformed microorganism comprising a nucleotide sequence selected from the group consisting of:

- a4
- (a) a nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 15, 17, 27, or 28;
 - (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 16, or 18;
 - (c) a nucleotide sequence characterized by at least 88% sequence identity to the nucleotide sequence set forth in (a);
 - (d) a nucleotide sequence encoding a protein comprising an amino acid sequence characterized by at least 85% sequence identity to the amino acid sequence set forth in (b);

- A4
- (e) ~~an antisense nucleotide sequence corresponding to a nucleotide sequence of any one of (a) to (d); and~~
 - (f) ~~a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of (a).~~

Sub B57 17. A method for impacting a plant pest comprising introducing into said plant or cell thereof at least one nucleotide construct comprising a coding sequence operably linked to a promoter that drives expression of a pesticidal polypeptide in plant cells, wherein said nucleotide sequence is selected from the group consisting of:

- A5
- (a) a nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 15, or 17;
 - (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 16, or 18;
 - (c) a nucleotide sequence characterized by at least 88% sequence identity to the nucleotide sequence set forth in (a);
 - (d) a nucleotide sequence encoding a protein comprising an amino acid sequence characterized by at least 85% sequence identity to the amino acid sequence set forth in (b);
 - (e) an antisense nucleotide sequence corresponding to a nucleotide sequence of any one of (a) to (d); and
 - (f) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of (a).

(amended)
18. The method according to claim 17, wherein the plant produces a polypeptide characterized by pesticidal activity against at least one pest of the order Coleoptera.

(amended)
19. The method according to claim 18, wherein said plant pest is selected from the group consisting of Colorado potato beetle, western corn rootworm, southern corn rootworm, and boll weevil.

a5 20. A variant of the nucleic acid set forth in SEQ ID NO:19 wherein the variant comprises a nucleotide sequence having at least one additional codon not present in the nucleotide sequence set forth in SEQ ID NO:19, wherein the at least one additional codon introduces an additional protease-sensitive site in the loop region between alpha-helices 3 and 4 of domain 1 of the encoded polypeptide, and further wherein the polypeptide encoded by the variant is characterized by improved pesticidal activity against a pest belonging to the order Coleoptera relative to the activity of the polypeptide set forth in SEQ ID NO:2.

a6 25. A variant of the nucleic acid set forth in SEQ ID NO: 15, wherein the variant comprises a nucleotide sequence that includes at least one additional codon that introduces an additional protease-sensitive site in the loop region between alpha-helices 3 and 4 of domain 1 of the polypeptide encoded by the variant nucleic acid, and further wherein the encoded polypeptide is characterized by improved pesticidal activity against a pest belonging to the order Coleoptera relative to the activity of the polypeptide set forth in SEQ ID NO: 2.

a7 29. A variant of the polypeptide set forth in SEQ ID NO: 16, wherein the variant comprises an amino acid sequence that includes at least one additional amino acid residue that introduces an additional protease-sensitive site in the loop region between alpha-helices 3 and 4 of domain 1 of the polypeptide, and further wherein the encoded polypeptide is characterized by improved pesticidal activity against a pest belonging to the order Coleoptera relative to the activity of the polypeptide set forth in SEQ ID NO:2.

a8 32. The transformed plant according to claim 31, wherein cells of the transformed plant express a polypeptide that is pesticidal for at least one pest belonging to the order Coleoptera.

Please add the following new claim:

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a⁹ 37. The transformed plant according to claim 32, wherein cells of the transformed plant express a polypeptide that is pesticidal for at least one pest selected from the group consisting of Colorado potato beetle, western corn rootworm, southern corn rootworm, and boll weevil.
